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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,243B

DATE: 02/26/2002

TIME: 14:04:01

Input Set : A:\010830-117.ST25.txt

Output Set: N:\CRF3\02262002\I840243B.raw

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4 <110> APPLICANT: MASTERNAK, Krzysztof
5      REITH, Walter
6      MACH, Bernard
8 <120> TITLE OF INVENTION: New Transcription Factor of MHC Class II Genes, Substances
9      Capable of Inhibiting This New Transcription Factor and
10     Medical Uses of These Substances
12 <130> FILE REFERENCE: 010830-117
14 <140> CURRENT APPLICATION NUMBER: US 09/840,243B
15 <141> CURRENT FILING DATE: 2001-04-24
17 <150> PRIOR APPLICATION NUMBER: EP 98120085.0
18 <151> PRIOR FILING DATE: 1998-10-24
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 40
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
32 <400> SEQUENCE: 1
33 ccgtacgcgt ctagaccatg gagcttaccc agcctgcaga                      40
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 31
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
44 <400> SEQUENCE: 2
45 ttcgaattct cgagtgtctg agtccccggc a                               31
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 37
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
56 <400> SEQUENCE: 3
57 ccgtacgcgt ctagaccatg gagcccactc aggttgc                        37
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 32
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

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68 <400> SEQUENCE: 4
69 ttcgaattct cgagtgcctg ggttccagca gg 32
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 30
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
80 <400> SEQUENCE: 5
81 ccagctctag actccaccac tctcaccaac 30
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 30
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
92 <400> SEQUENCE: 6
93 ccttcgaatt ctgctcttt tgccaggatg 30
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 30
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
104 <400> SEQUENCE: 7
105 ggttctctag attggcagca ctggggatag 30
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 30
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
116 <400> SEQUENCE: 8
117 gctacgaatt ccagcagaca cagccaaaac 30
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 69
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
128 <400> SEQUENCE: 9
129 ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct taccagcct 60
131 gcagaagac 69
134 <210> SEQ ID NO: 10
135 <211> LENGTH: 1345
136 <212> TYPE: DNA
137 <213> ORGANISM: Homo sapiens
139 <220> FEATURE:
140 <221> NAME/KEY: CDS

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141 <222> LOCATION: (418)..(1200)
143 <400> SEQUENCE: 10
144 acgcagggaa ggagggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60
146 ggctgggtgga gcgacaccca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120
148 cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180
150 actcccttct ttagccctct gccccgccc ttgcttataa gcctttgaga ccgcagaagg 240
152 gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300
154 gtttgccctc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360
156 gagagaactg ggctttcggc gcgggggggac agaggaggct cgtggggagc tttcccc 417
158 atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465
159 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
160 1 5 10 15
162 cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513
163 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
164 20 25 30
166 gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561
167 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
168 35 40 45
170 cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609
171 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
172 50 55 60
174 agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657
175 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
176 65 70 75 80
178 gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705
179 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
180 85 90 95
182 ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753
183 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
184 100 105 110
186 ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801
187 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
188 115 120 125
190 atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg 849
191 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
192 130 135 140
194 gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc 897
195 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
196 145 150 155 160
198 ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg 945
199 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
200 165 170 175
202 ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg 993
203 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
204 180 185 190
206 cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc 1041
207 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
208 195 200 205
210 ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac 1089

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211 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
212      210                      215                      220
214 acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag      1137
215 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
216 225                      230                      235                      240
218 gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc      1185
219 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
220                      245                      250                      255
222 gct gac cct gag tga aggccgcctg ccgggggactc agacactcag ggaacaaaat      1240
223 Ala Asp Pro Glu
224                      260
226 ggtcagccag agctgggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt      1300
228 gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag                      1345
231 <210> SEQ ID NO: 11
232 <211> LENGTH: 260
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 11
237 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
238      1                      5                      10                      15
240 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
241                      20                      25                      30
243 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
244                      35                      40                      45
246 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
247                      50                      55                      60
249 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
250      65                      70                      75                      80
252 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
253                      85                      90                      95
255 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
256                      100                     105                     110
258 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
259                      115                     120                     125
261 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
262                      130                     135                     140
264 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
265      145                     150                     155                     160
267 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
268                      165                     170                     175
270 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
271                      180                     185                     190
273 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
274                      195                     200                     205
276 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
277                      210                     215                     220
279 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
280      225                     230                     235                     240
282 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro

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```

283                               245                               250                               255
285 Ala Asp Pro Glu
286                               260
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 260
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 12
301 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
302   1                               5                               10                               15
304 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
305                               20                               25                               30
307 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
308                               35                               40                               45
310 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
311   50                               55                               60
313 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
314   65                               70                               75                               80
316 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
317                               85                               90                               95
319 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
320                               100                              105                              110
322 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
323                               115                              120                              125
325 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
326   130                              135                              140
328 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
329  145                              150                              155                              160
331 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
332                               165                              170                              175
334 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
335                               180                              185                              190
337 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
338                               195                              200                              205
340 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
341   210                              215                              220
343 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
344  225                              230                              235                              240
346 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
347                               245                               250                               255
349 Ala Asp Pro Glu
350                               260
353 <210> SEQ ID NO: 13
354 <211> LENGTH: 269
355 <212> TYPE: PRT
356 <213> ORGANISM: Murinae gen. sp.
358 <400> SEQUENCE: 13
359 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
360   1                               5                               10                               15

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/840,243B

DATE: 02/26/2002

TIME: 14:04:02

Input Set : A:\010830-117.ST25.txt

Output Set: N:\CRF3\02262002\I840243B.raw

L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18